

PCT09

RAW SEQUENCE LISTING

DATE: 11/14/2001

PATENT APPLICATION: US/09/869,565

TIME: 13:57:56

Input Set : A:\sequence listing ascii

Output Set: N:\CRF3\11142001\I869565.raw

7 <110> APPLICANT: Gardella, Thomas J.
 10 Kronenberg, Henry M.
 13 Potts Jr., John T.
 19 <120> TITLE OF INVENTION: PTH Receptor and Screening Assay Utilizing the Same
 25 <130> FILE REFERENCE: 0609.4730000
 29 <140> CURRENT APPLICATION NUMBER: 09/869,565
 C--> 32 <141> CURRENT FILING DATE: 1998-12-31 *2 Y*
 37 <150> PRIOR APPLICATION NUMBER: PCT/US98/27862
 40 <151> PRIOR FILING DATE: 1998-12-31
 46 <160> NUMBER OF SEQ ID NOS: 2
 52 <170> SOFTWARE: PatentIn Ver. 2.0
 58 <210> SEQ ID NO: 1
 61 <211> LENGTH: 1320
 64 <212> TYPE: DNA
 67 <213> ORGANISM: Artificial Sequence
 73 <220> FEATURE:
 76 <223> OTHER INFORMATION: Description of Artificial Sequence: cDNA
 82 <220> FEATURE:
 85 <221> NAME/KEY: CDS
 88 <222> LOCATION: (1)..(1308)
 94 <400> SEQUENCE: 1

97	atg ggg gcc gcc cgg atc gca ccc agc ctg gcg ctc cta ctc tgc tgc	48
100	Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Cys Cys	
103	1 5 10 15	
109	cca gtg ctc agc tcc gca tat gcg ctg gag gta ttt gac cgc cta ggc	96
112	Pro Val Leu Ser Ser Ala Tyr Ala Leu Glu Val Phe Asp Arg Leu Gly	
115	20 25 30	
121	atg atc tac acc gtg gga tac tcc atg tct ctc gcc tcc ctc acg gtg	144
124	Met Ile Tyr Thr Val Gly Tyr Ser Met Ser Leu Ala Ser Leu Thr Val	
127	35 40 45	
133	gct gtg ctc atc ctg gcc tat ttt agg cgg ctg cac tgc acg cgc aac	192
136	Ala Val Leu Ile Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn	
139	50 55 60	
145	tac atc cac atg cac atg ttc ctg tcg ttt atg ctg cgc gcc gcg agc	240
148	Tyr Ile His Met His Met Phe Leu Ser Phe Met Leu Arg Ala Ala Ser	
151	65 70 75 80	
157	atc ttc gtg aag gac gct gtg ctc tac tct ggc ttc acg ctg gat gag	288
160	Ile Phe Val Lys Asp Ala Val Leu Tyr Ser Gly Phe Thr Leu Asp Glu	
163	85 90 95	
169	gcc gag cgc ctc aca gag gaa gag ttg cac atc atc gcg cag gtg cca	336
172	Ala Glu Arg Leu Thr Glu Glu Glu Leu His Ile Ile Ala Gln Val Pro	
175	100 105 110	
181	cct ccg ccg gcc gct gcc gcc gta ggc tac gct ggc tgc cgc gtg gcg	384
184	Pro Pro Pro Ala Ala Ala Val Gly Tyr Ala Gly Cys Arg Val Ala	
187	115 120 125	
193	gtg acc ttc ttc ctc tac ttc ctg gct acc aac tac tac tgg atc ctg	432
196	Val Thr Phe Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu	

ENTERED

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199      130      135      140
205 gtg gag ggg ctg tac ttg cac agc ctc atc ttc atg gcc ttt ttc tca 480
208 Val Glu Gly Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser
211 145      150      155      160
217 gag aag aag tac ctg tgg ggc ttc acc atc ttt ggc tgg ggt cta ccg 528
220 Glu Lys Lys Tyr Leu Trp Gly Phe Thr Ile Phe Gly Trp Gly Leu Pro
223      165      170      175
229 gct gtc ttc gtg gct gtg tgg gtc ggt gtc aga gca acc ttg gcc aac 576
232 Ala Val Phe Val Ala Val Trp Val Gly Val Arg Ala Thr Leu Ala Asn
235      180      185      190
241 act ggg tgc tgg gat ctg agc tcc ggg cac aag aag tgg atc atc cag 624
244 Thr Gly Cys Trp Asp Leu Ser Ser Gly His Lys Lys Trp Ile Ile Gln
247      195      200      205
253 gtg ccc atc ctg gca tct gtt gtg ctc aac ttc atc ctt ttt atc aac 672
256 Val Pro Ile Leu Ala Ser Val Val Leu Asn Phe Ile Leu Phe Ile Asn
259      210      215      220
265 atc atc cgg gtg ctt gcc act aag ctt cgg gag acc aat gcg ggc cgg 720
268 Ile Ile Arg Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg
271 225      230      235      240
277 tgt gac acc agg cag cag tac cgg aag ctg ctc agg tcc acg ttg gtg 768
280 Cys Asp Thr Arg Gln Gln Tyr Arg Lys Leu Leu Arg Ser Thr Leu Val
283      245      250      255
289 ctc gtg ccg ctc ttt ggt gtg cac tac acc gtc ttc atg gcc ttg ccg 816
292 Leu Val Pro Leu Phe Gly Val His Tyr Thr Val Phe Met Ala Leu Pro
295      260      265      270
301 tac acc gag gtc tca ggg aca ttg tgg cag atc cag atg cat tat gag 864
304 Tyr Thr Glu Val Ser Gly Thr Leu Trp Gln Ile Gln Met His Tyr Glu
307      275      280      285
313 atg ctc ttc aac tcc ttc cag gga ttt ttt gtt gcc atc ata tac tgt 912
316 Met Leu Phe Asn Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys
319      290      295      300
325 ttc tgc aat ggt gag gtg cag gca gag att agg aag tca tgg agc cgc 960
328 Phe Cys Asn Gly Glu Val Gln Ala Glu Ile Arg Lys Ser Trp Ser Arg
331 305      310      315      320
337 tgg aca ctg gcg ttg gac ttc aag cgc aaa gca cga agt ggg agt agc 1008
340 Trp Thr Leu Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser
343      325      330      335
349 agc tac agc tat ggc cca atg gtg tct cac acg agt gtg acc aat gtg 1056
352 Ser Tyr Ser Tyr Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val
355      340      345      350
361 ggc ccc cgt gca gga ctc agc ctc ccc ctc agc ccc cgc ctg cct cct 1104
364 Gly Pro Arg Ala Gly Leu Ser Leu Pro Leu Ser Pro Arg Leu Pro Pro
367      355      360      365
373 gcc act acc aat ggc cac tcc cag ctg cct ggc cat gcc aag cca ggg 1152
376 Ala Thr Thr Asn Gly His Ser Gln Leu Pro Gly His Ala Lys Pro Gly
379      370      375      380
385 gct cca gcc act gag act gaa acc cta cca gtc act atg gcg gtt ccc 1200
388 Ala Pro Ala Thr Glu Thr Glu Thr Leu Pro Val Thr Met Ala Val Pro
391 385      390      395      400

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397 aag gac gat gga ttc ctt aac ggc tcc tgc tca ggc ctg gat gag gag      1248
400 Lys Asp Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu
403              405              410              415
409 gcc tcc ggg tct gcg cgg ccg cct cca ttg ttg cag gaa gga tgg gaa      1296
412 Ala Ser Gly Ser Ala Arg Pro Pro Pro Leu Leu Gln Glu Gly Trp Glu
415              420              425              430
421 aca gtc atg tga ctgggcacta gg                                  1320
424 Thr Val Met
427              435
436 <210> SEQ ID NO: 2
439 <211> LENGTH: 435
442 <212> TYPE: PRT
445 <213> ORGANISM: Artificial Sequence
451 <220> FEATURE:
454 <223> OTHER INFORMATION: Description of Artificial Sequence: rat protein sequence
455      that has been mutated in the laboratory, creating a
456      deletion in the original sequence.
461 <400> SEQUENCE: 2
464 Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Leu Cys Cys
467   1              5              10              15
473 Pro Val Leu Ser Ser Ala Tyr Ala Leu Glu Val Phe Asp Arg Leu Gly
476              20              25              30
482 Met Ile Tyr Thr Val Gly Tyr Ser Met Ser Leu Ala Ser Leu Thr Val
485              35              40              45
491 Ala Val Leu Ile Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn
494   50              55              60
500 Tyr Ile His Met His Met Phe Leu Ser Phe Met Leu Arg Ala Ala Ser
503   65              70              75              80
509 Ile Phe Val Lys Asp Ala Val Leu Tyr Ser Gly Phe Thr Leu Asp Glu
512              85              90              95
518 Ala Glu Arg Leu Thr Glu Glu Glu Leu His Ile Ile Ala Gln Val Pro
521              100              105              110
527 Pro Pro Pro Ala Ala Ala Ala Val Gly Tyr Ala Gly Cys Arg Val Ala
530              115              120              125
536 Val Thr Phe Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu
539              130              135              140
545 Val Glu Gly Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser
548 145              150              155              160
554 Glu Lys Lys Tyr Leu Trp Gly Phe Thr Ile Phe Gly Trp Gly Leu Pro
557              165              170              175
563 Ala Val Phe Val Ala Val Trp Val Gly Val Arg Ala Thr Leu Ala Asn
566              180              185              190
572 Thr Gly Cys Trp Asp Leu Ser Ser Gly His Lys Lys Trp Ile Ile Gln
575              195              200              205
581 Val Pro Ile Leu Ala Ser Val Val Leu Asn Phe Ile Leu Phe Ile Asn
584              210              215              220
590 Ile Ile Arg Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg
593 225              230              235              240
599 Cys Asp Thr Arg Gln Gln Tyr Arg Lys Leu Leu Arg Ser Thr Leu Val

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602                245                250                255
608 Leu Val Pro Leu Phe Gly Val His Tyr Thr Val Phe Met Ala Leu Pro
611                260                265                270
617 Tyr Thr Glu Val Ser Gly Thr Leu Trp Gln Ile Gln Met His Tyr Glu
620                275                280                285
626 Met Leu Phe Asn Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys
629                290                295                300
635 Phe Cys Asn Gly Glu Val Gln Ala Glu Ile Arg Lys Ser Trp Ser Arg
638 305                310                315                320
644 Trp Thr Leu Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser
647                325                330                335
653 Ser Tyr Ser Tyr Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val
656                340                345                350
662 Gly Pro Arg Ala Gly Leu Ser Leu Pro Leu Ser Pro Arg Leu Pro Pro
665                355                360                365
671 Ala Thr Thr Asn Gly His Ser Gln Leu Pro Gly His Ala Lys Pro Gly
674                370                375                380
680 Ala Pro Ala Thr Glu Thr Glu Thr Leu Pro Val Thr Met Ala Val Pro
683 385                390                395                400
689 Lys Asp Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu
692                405                410                415
698 Ala Ser Gly Ser Ala Arg Pro Pro Pro Leu Leu Gln Glu Gly Trp Glu
701                420                425                430
707 Thr Val Met
710                435

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VERIFICATION SUMMARY

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L:32 M:271 C: Current Filing Date differs, Replaced Current Filing Date